MYCOTAXON

ISSN (print) 0093-4666 (online) 2154-8889 Mycotaxon, Ltd. ©2018

*October–December 2018—Volume 133, pp. 643–654*

https://doi.org/10.5248/133.643

# *Cladosporium hebeiense* sp. nov., pathogenic on grape leaves in China

Cai-xia Wang[1,2,3], Wei Zhang[1,3], Mei Liu[1,3], Ji-ye Yan[1,3], Xing-hong Li[1,3*A], Yan-min Wei[2*B]

[1]*Institute of Plant & Environment Protection, Beijing Academy of Agriculture & Forestry Sciences, Haidian District, Beijing 100097, China*

[2]*Plant Science and Technology College, Beijing University of Agriculture, Changping District, Beijing 102206, China*

[3] *Beijing Key Laboratory of Environment Friendly Management on Fruit Diseases and Pests in North China, Haidian District, Beijing 100097, China*

* Correspondence to: [A] *lixinghong1962@163.com* & [B] *yanminwei@139.com*

Abstract—A new fungus in the *Cladosporium herbarum* complex, *Cladosporium hebeiense*, was isolated from leaf spots of *Vitis vinifera* in China. It produced short 0–1-septate ramoconidia that distinguished it from similar species. A multigene phylogenetic analysis based on the internal transcribed spacer region (ITS), partial translation elongation factor 1-alpha (TEF 1-α) gene, and the actin gene (ACT) supported *C. hebeiense* as separate from the closely related *C. ramotenellum*. Pathogenicity testing confirmed that *C. hebeiense* is a pathogen contributing to grape leaf spot disease.

Key words—*Cladosporiaceae, Capnodiales,* phylogeny, taxonomy,

## Introduction

*Cladosporium* Link is one of the largest and most heterogeneous hyphomycete genera encompassing more than 772 names (Dugan & al. 2004). These fungi are widely distributed throughout the world and have been isolated from plants, soil, food, textile, paint, and other organic materials (Bensch & al. 2012, 2015; Crous & al. 2014). Some *Cladosporium* species are capable of causing human and livestock diseases, and several, including *C. tenuissimum*

Cooke and *C. macrocarpum* Preuss, have been recorded as saprophytes from grapevines in China (Zhang 2003).

At present, several leaf spot diseases of grapevine have been reported in China, caused by *Sultanimyces vitiphyllus* (Speschnew) Videira & Crous (Fan & al. 2007, Song & al. 2014); *Pseudocercospora vitis* (Lév.) Speg. (Chai 2001) and *Passalora dissiliens* (Duby) U. Braun & Crous (Wang & al. 2002, Liang & al. 2010); *Acrospermum viticola* Ikata & Hitomi (Yao 2015); *Septoria ampelina* Berk. & M.A. Curtis, *Grovesinia moricola* (I. Hino) Redhead, and *Pseudopezicula tracheiphila* (Müll.-Thurg.) Korf & W.Y. Zhuang (Wang 2009); and *Neopestalotiopsis vitis* Jayaward. & al. (Jayawardena & al. 2016). Wilcox & al. (2015) have reported several additional grape leaf spot pathogens from other countries, e.g., *Briosia ampelophaga* Cavara, *Aureobasidium pullulans* (de Bary & Löwenthal) G. Arnaud, *Rhytisma vitis* Schwein., *Cladosporium viticola* Ces., *Asperisporium minutulum* (Sacc.) Deighton, and *Passalora heterosporella* U. Braun & Crous.

Here we describe a new *Cladosporium* pathogen, obtained from grape leaf spot in Hebei Province, China. Both morphological and molecular techniques were utilized to evaluate its taxonomic placement.

## Materials & methods

### Isolates & morphology

Grapevine leaf spot samples were collected from the greenhouse at Changli County, Hebei Province, China in 2016. All the symptomatic leaves were surface-sterilized with 70% ethanol for 1 min, then washed in sterilized water three times, and small pieces (<25 $mm^2$) of the diseased tissues were placed on potato dextrose agar (PDA) and incubated at 25°C in a 12–12 h light-dark artificial incubator until fungi were observed. Single spore isolations were used to obtain pure cultures as described in Chomnunti & al. (2014). The purified strains were re-cultured on PDA for 14 d at 25°C to observe colony morphologies (Sandoval-Denis & al. 2016). The conidia and conidiophores were photographed using an Axio Imager Z2 photographic microscope, and measurements were taken using ZEN PRO 2012 software. Thirty conidia were measured to calculate size range and average value. Living cultures of the two isolated strains were stored in the culture collection at Beijing Academy of Agricultural and Forestry Sciences, Beijing, China (JZB) and in Guizhou University Culture Collection, Guiyang, China (GUCC); the holotype specimen was conserved as a dried agar culture, in the Herbarium of Beijing Academy of Agricultural and Forestry Sciences (JZBL).

### DNA extraction & PCR amplification

Genome DNA was extracted according to Damm & al. (2008). Polymerase chain reactions (PCR) were conducted using C1000 Touch™ thermal Cycler according to

White & al. (1990) with gDNA as the template. The three genes amplified were the internal transcribed spacer region (ITS; using primers ITS4/ITS5, White & al. 1990), partial translation elongation factor 1-alpha gene (TEF 1-α; using primers TEF1-728F/TEF-2, O'Donnell & al. 1998), and the actin gene (ACT; using primers ACT-512F/ACT-783R, Bensch & al. 2012). The PCR conditions were as follows—for ITS: initial denaturation for 3 min at 94°C, followed by 34 cycles of denaturation for 30 s at 94°C, 30 s of annealing at 58°C, 90 s elongation at 72°C, and a final extension for 10 min at 72°C; for TEF 1-α and ACT: initial denaturation for 3 min at 94°C, followed by 40 cycles of denaturation for 30 s at 94°C, 30 s of annealing, 90 s elongation at 72°C, and a final extension for 10 min at 72°C. The annealing temperatures used in the cycling program were 54°C for TEF 1-α, and 52°C for ACT. Following PCR amplification, products were visualised on 1% agarose gel stained with ethidium bromide under UV light using a Gel Doc™ XR+ Molecular Imager. The PCR products were sequenced at Beijing Sunbiotech Co. Ltd.

**Phylogenetic analysis**

The sequences results were analyzed by BLASTn of National Center for Biotechnology Information (NCBI), and then the relevant reference sequences were downloaded from GenBank (Table 1). The ITS, TEF 1-α, and ACT sequences were aligned using MAFFT v.7 (Katoh & Toh 2008, http://mafft.cbrc.jp/alignment/server/), and manually aligned using BioEdit when necessary (Hall 1999). Then aligned sequences were converted into .nexus format using ALTER alignment online web tool (http://sing.ei.uvigo.es/ALTER/). Maximum parsimony (MP) analysis was conducted using Phylogenetic Analysis Using Parsimony (PAUP) v.4.0b10 (Swofford 2002). The phylogenetic tree was inferred using heuristic search option with tree bisection reconnection (TBR) branch swapping and 1000 random sequence additions, branches of zero length were collapsed and all parsimonious trees were saved. Descriptive statistics included tree length (TL), consistency index (CI), retention index (RI), rescaled consistence index (RC) and homoplasy index (HI). Bootstrap analyses (Hillis & Bull 1993) were based on 1000 replications.

Bayesian analyses were performed in MrBayes v.3.0b4 (Ronquist & Huelsenbeck 2003). The following models were applied: JC+G for the ITS gene region, TrNef+G for the TEF 1-α gene region and TrN+I+G model was selected for ACT gene. The Markov Chain Monte Carlo sampling (MCMC) analysis was conducted with four simultaneous Markov chains. They were run for 1,000,000 generations; sampling the trees at every 100th generation. From the 10,000 trees obtained, the first 2000 representing the burn-in phase were discarded. The remaining 8000 trees were used to calculate posterior probabilities in the majority rule consensus tree (critical value for the topological convergence diagnostic set to 0.01) (Crous & al. 2006). Sequences derived in this study have been deposited in GenBank (Table 1).

**Pathogenicity test**

Young and healthy detached *Vitis vinifer*a L. 'Summer Black' leaves collected from the greenhouse were used to test for pathogenicity. Leaves were disinfected with 75%

Table 1. Sequences of *Cladosporium* used in the molecular analyses.

| Species | Isolate | GenBank accession numbers | | | Reference |
|---|---|---|---|---|---|
| | | ITS | TEF1-α | ACT | |
| *C. aggregatocicatricatum* | CBS 140493 | KT600448 | KT600547 | KT600645 | Bensch & al. 2015 |
| *C. allicinum* | CBS 121624 | EF679350 | EF679425 | EF679502 | Schubert & al. 2007 |
| *C. allii* | CBS 101.81 | JN906977 | JN906983 | JN906996 | Bensch & al. 2012 |
| *C. angustiherbarum* | CBS 140479 | KT600378 | KT600475 | KT600574 | Bensch & al. 2015 |
| *C. antarcticum* | CBS 690.92 | EF679334 | EF679405 | EF679484 | Schubert &al. 2007 |
| *C. arthropodii* | CBS 124043 | JN906979 | JN906985 | JN906998 | Bensch & al. 2012 |
| *C. basiinflatum* | CBS 822.84 | HM148000 | HM148241 | HM148487 | Bensch &al. 2010 |
| *C. echinulatum* | CBS 123191 | JN906980 | JN906987 | JN906999 | Bensch & al. 2012 |
| *C. floccosum* | CBS 140463 | LN834416 | LN834512 | LN834600 | Sandoval-Denis & al. 2016 |
| *C. herbaroides* | CBS 121626 | EF679357 | EF679432 | EF679509 | Schubert & al. 2009 |
| *C. herbarum* | CBS 121621 | EF679363 | EF679440 | EF679516 | Schubert & al. 2009 |
| *C. iridis* | CBS 138.40 | EF679370 | EF679447 | EF679523 | Schubert & al. 2009 |
| *C. limoniforme* | CBS 113737 | KT600396 | KT600493 | KT600591 | Bensch & al. 2015 |
| *C. macrocarpum* | CBS 121623 | EF679375 | EF679453 | EF679529 | Schubert & al. 2009 |
| *C. ossifragi* | CBS 842.91 | EF679381 | EF679459 | EF679535 | Schubert & al. 2009 |
| *C. paralimoniforme* | CGMCC3.18103 | KX938393 | KX938409. | KX938376 | Ma & al. 2017 |

| | | | | | |
|---|---|---|---|---|---|
| *C. phlei* | CBS 358.69 | JN906981 | JN906991 | JN907000 | Bensch & al. 2012 |
| *C. prolongatum* | CGMCC3.18035 | KX938395 | KX938411 | KX938378 | Ma & al. 2017 |
| *C. pseudiridis* | CBS 116463 | EF679383 | EF679461 | EF679537 | Schubert & al. 2009 |
| *C. ramotenellum* | CBS 121628 | EF679384 | EF679462 | EF679538 | Schubert & al. 2007 |
| *C. rhoicola* | CBS 140492 | KT600440 | KT600539 | KT600637 | Bensch & al. 2015 |
| *C. sinuosum* | CBS 121629 | EF679386 | EF679464 | EF679540 | Schubert & al. 2007 |
| *C. soldanellae* | CPC 13153 | JN906982 | JN906994 | JN907001 | Bensch & al. 2012 |
| *C. spinulosum* | CBS 119907 | EF679388 | EF679466 | EF679542 | Schubert & al. 2007 |
| *C. subinflatum* | CBS 121630 | EF679389 | EF679467 | EF679543 | Schubert & al. 2007 |
| *C. subtilissimum* | CBS 113754 | EF679397 | EF679475 | EF679551 | Schubert & al. 2007 |
| *C. tenellum* | CBS 121634 | EF679401 | EF679479 | EF679555 | Schubert & al. 2007 |
| *C. tuberosum* | CBS 140693 | LN834417 | LN834513 | LN834601 | Sandoval-Denis & al. 2016 |
| *C. variabile* | CBS 121635 | EF679402 | EF679480 | EF679556 | Schubert & al. 2007 |
| *C. verruculosum* | CGMCC3.18099 | KX938389 | KX938405 | KX938372 | Ma & al. 2017 |
| *C. **hebeiense*** | **JZB390001** [T] | **MG516597** | **MG516595** | **MG516593** | **This paper** |
| | **JZB390005** | **MG516598** | **MG516596** | **MG516594** | **This paper** |
| *C. colombiae* | CBS 274.80B | FJ936159 | FJ936163 | FJ936166 | Schubert & al. 2009 |
| *C. langeronii* | CBS 189.54 | DQ780379 | JN906990 | EF101357 | Zalar & al. 2007 |

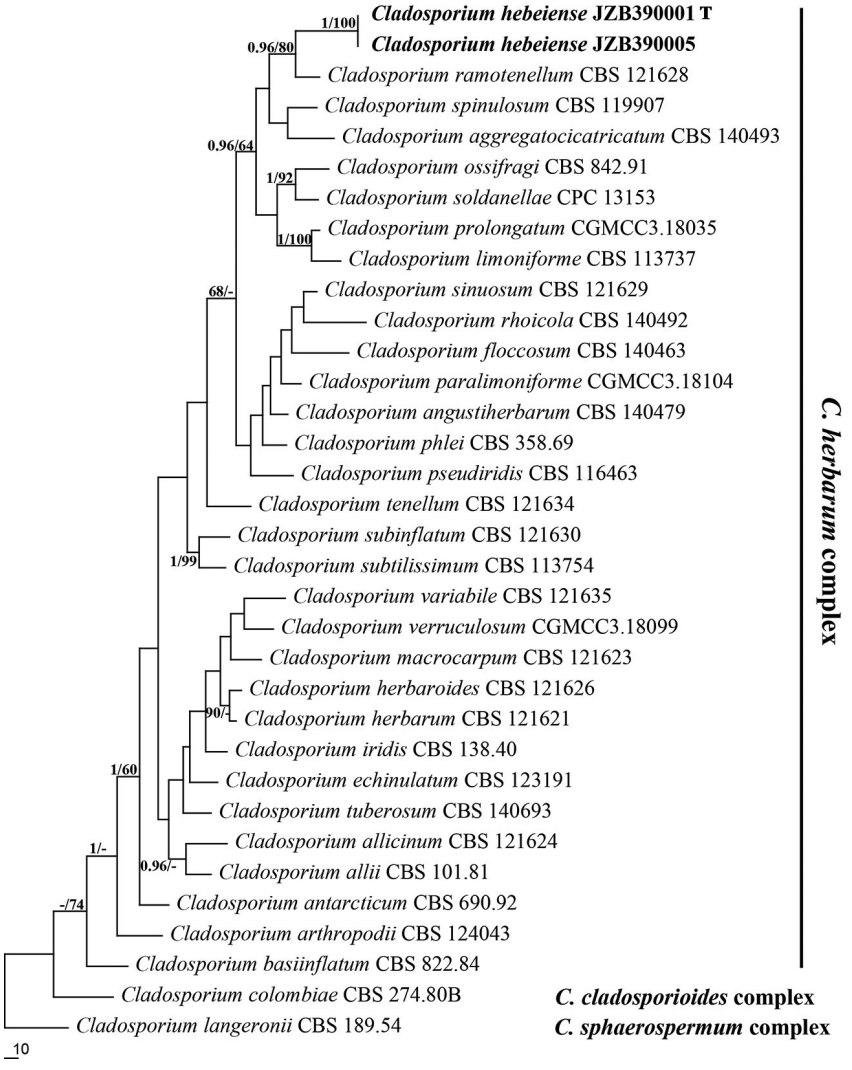


Fig. 1. Phylogram based on maximum parsimony and Bayesian analyses with combined ITS, TEF1-α, and ACT sequence data of *Cladosporium* species. Bootstrap values >50% and posterior probabilities >0.96 are indicated near the nodes. Sequences from our new species are set in bold font. The scale bar indicates 10 changes. The tree is rooted with *C. langeronii* [*C. sphaerospermum* complex] and *C. colombiae* [*C. cladosporioides* complex].

alcohol for 30 s, washed with sterile water 3 times, and then placed in sterile operating platform for drying. We re-cultured the isolates on PDA for 7 d, prepared a $1 \times 10^5$/ml spore suspension, and conducted the pathogenicity test using three leaves per isolate with the drip method. Leaves were inoculated using two inoculation methods: non-wounded and wounded, with 4 inoculation points on each leaf (2 inoculation points on each side) with a spore suspension of 20 µl. Inoculated leaves were placed into an inoculation box for moisturizing, and the box was placed in an incubator at 25°C for 12 h light/12 h dark. The pathogenic experiment was repeated 3 times, with sterile water serving as the negative control. After the onset of disease symptoms, the fungus was re-isolated, fulfilling Koch's postulates.

### Phylogenetic results

The phylogenetic tree constructed by MP comprised 30 sequences from the *Cladosporium herbarum* complex (Bensch & al. 2012, 2015), with *Cladosporium langeronii* (CBS 189.54; *C. sphaerospermum* complex) and *C. colombiae* (CBS 274.80B; *C. cladosporioides* complex) as the outgroup. After the three gene regions (ITS, TEF 1-α, and ACT) were combined, the final alignment was 1048 characters long (ITS: 1–478, TEF 1-α: 479–859, ACT: 860–1048). The concatenated alignment contained 229 parsimony informative characters, 707 constant characters, and 112 variable and parsimony uninformative characters. One (TL = 1259, CI = 0.448, RI = 0.529, RC = 0.237, HI = 0.552) of 1000 equally parsimonious trees is shown in Fig. 1. Within the *Cladosporium herbarum* complex, our two isolates (JZB390001, JZB390005) clustered together with maximum parsimony bootstrap (MP) = 100% and Bayesian posterior probability (PP) = 1. Our isolates clustered with their sister taxon, *C. ramotenellum* K. Schub. & al. with MP = 80% and PP = 0.96.

### Taxonomy

***Cladosporium hebeiense*** C.X. Wang, Xing H. Li & Yan M. Wei, **sp. nov.** Fig. 2

Index Fungorum IF553970

Differs from *Cladosporium ramotenellum* by its shorter, wider ramoconidia with fewer septa.

Type: China, Hebei Province, Changli County, on leaf spot of greenhouse *Vitis vinifera* (*Vitaceae*), November 2016, Xinghong Li (Holotype, JZBL390001; ex-holotype cultures, JZB390001, GUCC3075; GenBank MG516597, MG516595, MG516593).

Etymology: Referring to the collection locality in Hebei Province.

Colonies: On PDA 45–55 mm diam after 14 d at 25°C, moderate green to dark green, flat to umbonate and slightly folded, velvety with white cottony centre and regular margin; reverse olive brown. On OA 43–47 mm diam after

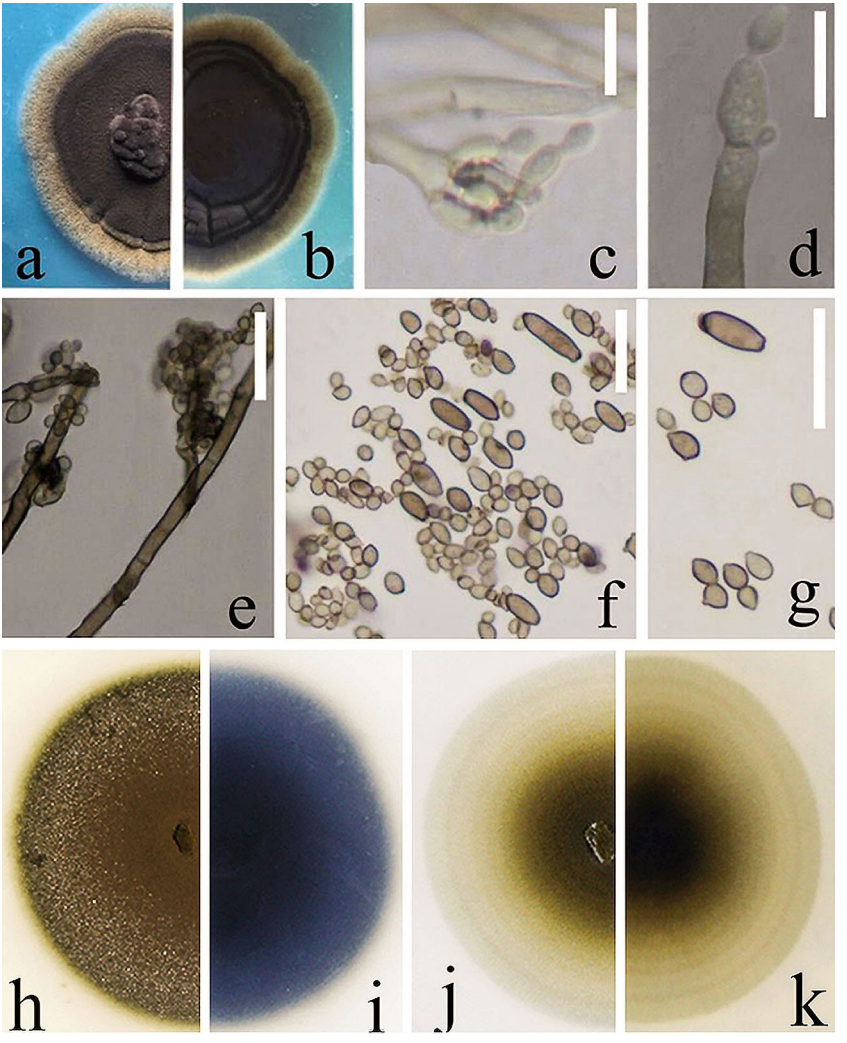


Fig. 2. *Cladosporium hebeiense* (JZB3900005, ex-holotype). a, b. Colonies on PDA (a-obverse, b-reverse) at 25°C; c, d. Sporulation with primary conidia on PDA; e. Conidiophores and conidia on PDA; f, g. Two kinds of conidia on PDA; h, i. Colonies on OA (a = obverse, b = reverse) at 25°C; j, k. Colonies on SNA (a = obverse, b = reverse) at 25°C. Scale bars: c, e, f = 5 μm; d, g = 10 μm.

14 d at 25°C, olive green or olive brown, nearly round, powdery, reverse dark olive green to black. On SNA 32–34 mm diam after 14 d at 25°C, yellowish-brown to dark brown, aerial hyphae not obvious, nearly round, reverse back

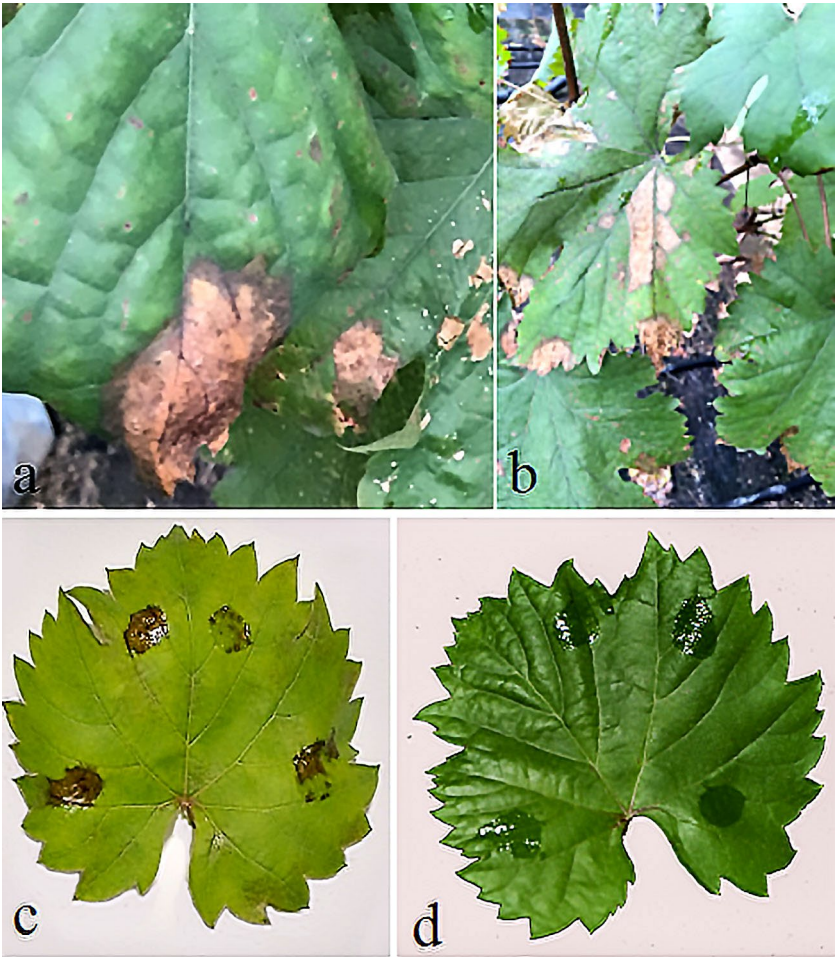


Fig. 3. Symptoms of grape leaf spot disease associated with *Cladosporium hebeiense*. a, b. Field symptoms of grape leaf spot; c. Symptoms on in vitro grape leaves, 7 d after inoculation with isolate JZB3900001. d. In vitro grape leaves, 7 d after control inoculation with sterile water.

brown to dark brown. Mycelium superficial and immersed, hyphae septate, branched, 1.5–3 µm wide, sub-hyaline to pale brown, smooth. Conidiophores erect, flexuous, sub-cylindrical, septate, mostly unbranched, ≤150 × 3–3.5 µm, pale to medium olivaceous brown, smooth. Conidiogenous cells terminal, cylindrical, nodulose, 18–20 × 3–4.5 µm, smooth and thick-walled, bearing up to 2–3 conspicuous, refractive, slightly darkened conidiogenous loci of 2–2.5

μm diam. Ramoconidia 0–1-septate, subcylindrical to cylindrical, 7.5–20 × 4–5.5 μm (mean = 10.24 × 4.54 μm, n = 30), smooth or finely verruculose. Conidia forming branched chains with ≤5–7 conidia at the unbranched terminus, pale green-brown, smooth- and thick-walled, with protuberant and darkened conidial hila; small terminal conidia aseptate, obovoidal to short ellipsoidal, 3–8 × 3–5 μm (mean = 5.48 × 3.88 μm, n = 30).

Additional material examined: **China**, **Hebei Province**, **Changli County**, on leaf spot of greenhouse *Vitis vinifera*, November 2016, Xinghong Li (cultures (JZB390005, GUCC3076; GenBank MG516598, MG516596, MG516594).

### Pathogenicity

This grape leaf spot is primarily characterized as light brown spots with a darker edge, circular, oval, or irregular in shape, mainly concentrated in the relatively old leaves (Fig. 3). The leaves begin to show symptoms at 3 d. Symptoms were similar to those of field acquired leaf spot disease at 7 d. No symptoms were observed on the control (Fig. 3). After Koch's postulates, re-isolated cultures, and morphological observation of ramoconidia and conidia confirmed the pathogen was *Cladosporium hebeiense*.

### Discussion

As can be seen from the phylogenetic tree (Fig. 1), *Cladosporium hebeiense* falls within the *C. herbarum* complex and is closely related to *C. ramotenellum* with strong support (MP = 80%, PP = 0.96). However, *C. ramotenellum* differs from *C. hebeiense* by its longer, narrower ramoconidia with more numerous septa (<47 × 2–4 μm, 0–1(–4)-septate; Bensch & al. 2012, Schubert & al. 2007). Based on morphological comparison and phylogenetic analysis, we confirm that *C. hebeiense* is a new taxon in the *C. herbarum* complex.

*Cladosporium* species are very common fungi that cause leaf spot diseases in many plants such as rock lily, wheat, *Vigna umbellata, Citrus sinensis,* and *Colocasia esculenta* (Bensch & al. 2012, Sandoval-Denis & al. 2016). However, at present there are no other reports from China of grape leaf spots caused by *Cladosporium*. Our report not only adds a new *Cladosporium* species, but also promotes the research progress of grape leaf spot in China. Our next step will be to investigate the main grape producing areas in China to evaluate the impact of *C. hebeiense* on Chinese grapes.

#### Acknowledgments

The project was funded by CARS-29-bc-2. We thank Ishara Manawasinghe and Thilini Chethana for experimental guidance and would like to acknowledge

Dr. Ruvishika Jayawardena and Dr. Yong Wang for reviewing content of the manuscript.

**Literature cited**

Bensch K, Groenewald JZ, Dijksterhuis J, Starink-Willemse M, Andersen B & al. 2010. Species and ecological diversity within the *Cladosporium cladosporioides* complex (*Davidiellaceae*, *Capnodiales*). Studies in Mycology 67. 94 p. https://doi.org/10.3114/sim.2010.67.01

Bensch K, Braun U, Groenewald J-Z, Crous PW. 2012. The genus *Cladosporium*. Studies in Mycology 72. 401 p. https://doi.org/10.3114/sim0003

Bensch K, Groenewald JZ, Braun U, Dijksterhuis J, de Jesús Yáñez-Morales M, Crous PW. 2015. Common but different: the expanding realm of *Cladosporium*. Studies in Mycology 82: 23–74. https://doi.org/10.1016/j.simyco.2015.10.001

Chai ZX. 2001. Identification of grape brown spot in Lanzhou Area. Journal of Gansu Agricultural University 36(1): 61–64 (in Chinese). https://doi.org/10.13432/j.cnki.jgsau.2001.01.010

Chomnunti P, Hongsanan S, Aguirre-Hudson B, Tian Q, Peršoh D & al. 2014. The sooty moulds. Fungal Diversity 66: 1–36. https://doi.org/10.1007/s13225-014-0278-5

Crous PW, Slippers B, Wingfield MJ, Rheeder J, Marasas WFO, Phillips AJL, Alves A, Burgess TI, Barber PA, Groenewald JZ. 2006. Phylogenetic lineages in the *Botryosphaeriaceae*. Studies in Mycology 55: 235–253. https://doi.org/10.3114/sim.55.1.235

Crous PW, Shivas RG, Quaedvlieg W, van der Bank M, Zhang Y, Summerell BA & al. 2014. Fungal Planet description sheets: 214–280. Persoonia 32: 184–306. https://doi.org/10.3767/003158514X682395

Damm U, Mostert L, Crous PW, Fourie PH. 2008. Novel *Phaeoacremonium* species associated with necrotic wood of *Prunus* trees. Persoonia 20: 87–102. https://doi.org/10.3767/003158508X324227

Dugan FM, Schubert K, Braun U. 2004. Check-list of *Cladosporium* names. Schlechtendalia 11. 103 p.

Fan YM, Hao JZ, Zhang MZ, Zhao ZY, Wang HQ, Wu YH, Zhang J. 2007. Pathogen identification and symptom identification of grape brown stripe disease in Xinjiang. Plant Protection 3(3): 140–142 (in Chinese). https://doi.org/10.3969/j.issn.0529-1542.2007.03.042.

Hall TA. 1999. BioEdit: a user-friendly biological sequence alignment editor and analysis program for Windows 95/98/NT. Nucleic Acids Symposium Series 41: 95–98.

Hillis DM, Bull JJ. 1993. An empirical test of bootstrapping as a method for assessing confidence in phylogenetic analysis. Systematic Biology 42: 182–192. https://doi.org/10.1093/sysbio/42.2.182

Jayawardena RS, Liu M, Maharachchikumbura SSN, Zhang W, Xing QK, Hyde KD, Nilthong S, Li XH, Yan JY. 2016. *Neopestalotiopsis vitis* sp. nov. causing grapevine leaf spot in China. Phytotaxa 258(1): 63–74. https://doi.org/10.11646/phytotaxa.258.1.4

Katoh K, Toh H. 2008. Recent developments in the MAFFT multiple sequence alignment program. Brief. Bioinform. 9: 286–298. https://doi.org/10.1093/bib/bbn013

Liang CH, Zhao KH, Liu CY, Wang L. 2010. Advances in research on grape brown spot. Liaoning Agricultural Sciences 117–119 (in Chinese).

Ma R, Chen Q, Fan YL, Wang Q, Chen SF, Liu XZ, Cai L, Yao B. 2017. Six new soil–inhabiting *Cladosporium* species from plateaus in China. Mycologia 109: 244-260. https://doi.org/10.1080/00275514.2017.1302254

O'Donnell K, Kistler HC, Cigelnik E, Ploetz RC. 1998. Multiple evolutionary origins of the fungus causing Panama disease of banana: concordant evidence from nuclear and mitochondrial gene genealogies. Proceedings of the National Academy of Sciences of the United States of America 95(5): 2044–2049. https://doi.org/10.1073/pnas.95.5.2044

Ronquist F, Huelsenbeck JP. 2003. MrBayes 3: Bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572. http://doi.org/10.1093/bioinformatics/btg180

Sandoval-Denis M, Gené J, Sutton DA, Wiederhold NP, Cano-Lira JF, Guarro J. 2016. New species of *Cladosporium* associated with human and animal infections. Persoonia, 36: 281–298. https://doi.org/10.3767/003158516X691951

Schubert K, Groenewald JZ, Braun U, Dijksterhuis J, Starink MS, Hill CF, Zalar P, de Hoog GS, Crous PW. 2007. Biodiversity in the *Cladosporium herbarum* complex (*Davidiellaceae*, *Capnodiales*), with standardisation of methods for *Cladosporium* taxonomy and diagnostics. Studies in Mycology 58: 105–156. https://doi.org/10.3114/sim.2007.58.05

Schubert K, Greslebin A, Groenewald JZ, Crous PW. 2009. New foliicolous species of *Cladosporium* from South America. Persoonia 22: 111–122. https://doi.org/10.3767/003158509X449381

Song WC, Guo QY, Wang HK, Wang DD, Lei D, Liu Y, Alaiyi. 2014. Grape common diseases and their occurrence status quo in Turpan and some other areas in Northern Xinjiang. Xinjiang Agricultural Sciences 51(5): 893–901 (in Chinese).

Swofford DL. 2002. PAUP* 4.0: phylogenetic analysis using parsimony (* and other methods). Sinauer Associates, Sunderland.

Wang ZY. 2009. Chinese grape diseases and insect pests and integrated control techniques. China Agriculture Press, Beijing, China (in Chinese).

Wang GZ, Fan ZQ, Ru QH, An HW. 2002. Survey of grapevine diseases in Donglu, Helan mountain, Ningxia. Northern Horticulture (6): 64–65 (in Chinese).

White TJ, Bruns T, Lee S, Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: MA & al. (eds). PCR protocols: a guide to methods and applications. Academic Press, New York, USA. https://doi.org/10.1016/b978-0-12-372180-8.50042-1

Wilcox WF, Gubler WD, Uyemoto JK. 2015. Compendium of grape diseases, disorders, and pests. The American Phytopathological Society Press.

Yao M. 2015. Identification and control of two leaf diseases in grape. Journal of Agricultural Catastrophology 5(9): 5–6, 10 (in Chinese).

Zalar P, de Hoog GS, Schroers HJ, Crous PW, Groenewald JZ, Gunde-Cimerman N. 2007. Phylogeny and ecology of the ubiquitous saprobe *Cladosporium sphaerospermum*, with descriptions of seven new species from hypersaline environments. Studies in Mycology 58: 157–183. https://doi.org/10.3114/sim.2007.58.06

Zhang TY. 2003. Flora Fungorum Sinicorum, vol.14. *Cladosporium*, *Fusicladium*, *Pyricularia*. Science Press, Beijing, China. (in Chinese).